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L2 ANSWER 2 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
ACCESSION NUMBER: 2002:700274 CAPLUS
TITLE: The stress-response sigma factor .sigma.h controls the expression of ssgB, a homologue of the sporulation-specific cell division gene **ssgA** , in streptomyces coelicolor A3(2)
AUTHOR(S): Kormanec, J.; Sevcikova, B.
CORPORATE SOURCE: Institute of Molecular Biology, Slovak Academy of Sciences, Bratislava, 842 51, Slovakia
SOURCE: Molecular Genetics and Genomics (2002), 267(4), 536-543
CODEN: MGGOAA; ISSN: 1617-4615
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal; Miscellaneous
LANGUAGE: English
AB By using a previously established method for the identification of promoters recognized by a particular sigma factor of RNA polymerase, we identified a promoter in Streptomyces coelicolor A3(2) that is recognized by a heterologous RNA polymerase contg. the late sporulation-specific sigma factor .sigma.F. The promoter directed the expression of a gene named ssgB, which is related to the sporulation-specific cell division gene **ssgA**. These genes, together with three others, constitute a new family of paralogous genes specific for Streptomyces. S1-nuclease mapping using RNA prepd. from an Escherichia coli strain that expresses ssgB under the control of .sigma.F, and from S. coelicolor A3(2) at various developmental stages, identified identical transcription start points in both strains, corresponding to the promoter ssgBp. The promoter is developmentally regulated in S. coelicolor: it is induced at the time of aerial mycelium formation and is most active during sporulation. However, the level of the ssgB transcript was unaffected in a sigF mutant of S. coelicolor A3(2). Interestingly, the level of the transcript was substantially reduced in an S. coelicolor strain that was mutant for the sigH gene, which encodes a stress-response sigma factor (.sigma.H) that is essential for sporulation in S. coelicolor A3(2). This dependence of ssgB upon sigH was confirmed by an in vitro transcription assay, in which .sigma.H, in the presence of the S. coelicolor core RNA polymerase, was able to recognize ssgBp. These results suggest that the S. coelicolor ssgB gene is under the control of the stress-response .sigma.H. Transcription of ssgB was investigated in S. coelicolor A3(2) mutants with lesions in each of six known early whi genes required for sporulation septation. Expression of ssgB was deregulated in three of the mutants (whiA, whiI, and whiJ). Based on these data, it is proposed that the ssgB gene product plays a role in the developmental process in S. coelicolor A3(2).
REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 1 OF 20 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2002:944103 SCISEARCH
THE GENUINE ARTICLE: 614ZL
TITLE: Protein analysis in a pleomorphically deteriorated strain of the insect-pathogenic fungus Metarhizium anisopliae
AUTHOR: Kamp A M; Bidochka M J (Reprint)
CORPORATE SOURCE: Brock Univ, Dept Biol Sci, St Catharines, ON L2S 3A1, Canada (Reprint)
COUNTRY OF AUTHOR: Canada
SOURCE: CANADIAN JOURNAL OF MICROBIOLOGY, (SEP 2002) Vol. 48, No. 9, pp. 787-792.
Publisher: NATL RESEARCH COUNCIL CANADA, RESEARCH JOURNALS, MONTREAL RD, OTTAWA, ONTARIO K1A 0R6, CANADA.
ISSN: 0008-4166.
DOCUMENT TYPE: Article; Journal

LANGUAGE: English
REFERENCE COUNT: 14
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Pleomorphic deterioration is a process where a fungal isolate loses the ability to produce conidia during repeated subculturing. We have previously isolated strains of the entomopathogenic fungus Metarhizium anisopliae that have irreversibly lost the ability to produce conidia and only produce mycelia when grown on agar. Gel electrophoresis was used to examine differences in intracellular protein patterns (urea-soluble proteins and urea-insoluble proteins (i.e. hydrophobins)) in conidating and mycelial cultures of M. anisopliae. Two major proteins present in a conidiating culture and one from a mycelial culture were N-terminally sequenced but showed no homologies to known proteins. The presence of hydrophobins in conidating and mycelial cultures was also examined, and it was shown that these proteins were abundant in conidiating cultures but not in mycelial cultures. We also used primers designed from regulatory genes involved in conidiation in Aspergillus nidulans. The amplified fragments were not homologous to A. nidulans genes.

L2 ANSWER 2 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
ACCESSION NUMBER: 2002:700274 CAPLUS
TITLE: The stress-response sigma factor .sigma.h controls the expression of ssgB, a homologue of the sporulation-specific cell division gene **ssgA**, in streptomyces coelicolor A3(2)
AUTHOR(S): Kormanec, J.; Sevcikova, B.
CORPORATE SOURCE: Institute of Molecular Biology, Slovak Academy of Sciences, Bratislava, 842 51, Slovakia
SOURCE: Molecular Genetics and Genomics (2002), 267(4), 536-543
CODEN: MGGOAA; ISSN: 1617-4615
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal; Miscellaneous
LANGUAGE: English

AB By using a previously established method for the identification of promoters recognized by a particular sigma factor of RNA polymerase, we identified a promoter in Streptomyces coelicolor A3(2) that is recognized by a heterologous RNA polymerase contg. the late sporulation-specific sigma factor .sigma.F. The promoter directed the expression of a gene named ssgB, which is related to the sporulation-specific cell division gene **ssgA**. These genes, together with three others, constitute a new family of paralogous genes specific for Streptomyces. S1-nuclease mapping using RNA prepd. from an Escherichia coli strain that expresses ssgB under the control of .sigma.F, and from S. coelicolor A3(2) at various developmental stages, identified identical transcription start points in both strains, corresponding to the promoter ssgBp. The promoter is developmentally regulated in S. coelicolor: it is induced at the time of aerial mycelium formation and is most active during sporulation. However, the level of the ssgB transcript was unaffected in a sigF mutant of S. coelicolor A3(2). Interestingly, the level of the transcript was substantially reduced in an S. coelicolor strain that was mutant for the sigH gene, which encodes a stress-response sigma factor (.sigma.H) that is essential for sporulation in S. coelicolor A3(2). This dependence of ssgB upon sigH was confirmed by an in vitro transcription assay, in which .sigma.H, in the presence of the S. coelicolor core RNA polymerase, was able to recognize ssgBp. These results suggest that the S. coelicolor ssgB gene is under the control of the stress-response .sigma.H. Transcription of ssgB was investigated in S. coelicolor A3(2) mutants with lesions in each of six known early whi genes required for sporulation septation. Expression of ssgB was deregulated in three of the mutants (whiA, whiI, and whiJ). Based on these data, it is proposed that the ssgB gene product plays a role in the developmental process in S. coelicolor A3(2).

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 20 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2001:820695 SCISEARCH
THE GENUINE ARTICLE: 481CL
TITLE: Simultaneous and multi-criteria optimization of TS requirements and maintenance at NPPs
AUTHOR: Martorell S (Reprint); Sanchez A; Carlos S; Serradell V
CORPORATE SOURCE: Univ Politecn Valencia, Dept Chem & Nucl Engn, POB 22012, Valencia 46071, Spain (Reprint); Univ Politecn Valencia, Dept Chem & Nucl Engn, Valencia 46071, Spain; Univ Politecn Valencia, Dept Stat & Operat Res, Valencia 46071, Spain
COUNTRY OF AUTHOR: Spain
SOURCE: ANNALS OF NUCLEAR ENERGY, (JAN 2002) Vol. 29, No. 2, pp. 147-168.
Publisher: PERGAMON-ELSEVIER SCIENCE LTD, THE BOULEVARD, LANGFORD LANE, KIDLINGTON, OXFORD OX5 1GB, ENGLAND.
ISSN: 0306-4549.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 48

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB One of the main concerns of the nuclear industry is to improve the availability of safety-related systems at nuclear power plants (NPPs) to achieve high safety levels. The development of efficient testing and maintenance has been traditionally one of the different ways to guarantee high levels of systems availability, which are implemented at NPP through technical specification and maintenance requirements (TS&M). On the other hand, there is a widely recognized interest in using the probabilistic risk analysis (PRA) for risk-informed applications aimed to emphasize both effective risk control and effective resource expenditures at NPPs. TS&M-related parameters in a plant are associated with controlling risk or with satisfying requirements, and are candidate to be evaluated for their resource effectiveness in risk-informed applications. The resource versus risk-control effectiveness principles formally enter in optimization problems where the cost or the burden for the plant staff is to be minimized while the risk or the availability of the safety equipment is constrained to be at a given level, and vice versa. Optimization of TS&M has been found interesting from the very beginning. However, the resolution of such a kind of optimization problem has been limited to focus on only individual TS&M-related parameters (STI, ACT, PM frequency, etc.) and/or adopting an individual optimization criterion (availability, costs, plant risks, etc.). Nevertheless, a number of reasons exist (e.g. interaction, similar scope, etc.) that justify the growing interest in the last years to focus on the simultaneous and multi-criteria optimization of TS&M. In the simultaneous optimization of TS&M-related parameters based on risk (or unavailability) and cost, like in many other engineering optimization problems, one normally faces multi-modal and non-linear objective functions and a variety of both linear and non-linear constraints. Genetic algorithms (GAs) have proved their capability to solve these kinds of problems, although GAs are essentially unconstrained optimization techniques that require adaptation for the intended constrained optimization, where TS&M-related parameters act as the decision variables. This paper encompasses, in Section 2, the problem formulation where the objective function is derived and constraints that apply in the simultaneous and multi-criteria optimization of TS&M activities based on risk and cost functions at system level. Fundamentals of a steady-state GA (**SSGA**) as an optimization method is given in Section 3, which satisfies the above requirements, paying special attention to its use in constrained optimization problems. A simple case of application is provided in Section 4, focussing on TS&M-related parameters optimization for a stand-by safety-related system, which demonstrates how the **SSGA**-based optimization approach works at

the system level, providing practical and complete alternatives beyond only mathematical solutions to a particular parameter. Finally, Section 5 presents our conclusions. (C) 2001 Elsevier Science Ltd. All rights reserved.

L2 ANSWER 4 OF 20 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2002:947738 SCISEARCH
THE GENUINE ARTICLE: 616BT
TITLE: Deprogrammed sporulation in Streptomyces
AUTHOR: Ohnishi Y; Seo J W; Horinouchi S (Reprint)
CORPORATE SOURCE: Univ Tokyo, Grad Sch Agr & Life Sci, Dept Biotechnol, Bunkyo Ku, Tokyo 1138657, Japan (Reprint)
COUNTRY OF AUTHOR: Japan
SOURCE: FEMS MICROBIOLOGY LETTERS, (29 OCT 2002) Vol. 216, No. 1, pp. 1-7.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0378-1097.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 23

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The bacterial genus Streptomyces forms chains of spores by septation at intervals in aerial hyphae and subsequent maturation on solid medium. Substrate hyphae undergo extensive lysis, liberating nutrients on which aerial hyphae develop. Some mutant strains, however, ectopically form spores by septation in substrate hyphae on solid medium or in vegetative hyphae in liquid medium, which suggests that all hyphae have the potential to differentiate into spores. A Streptomyces griseus mutant strain NP4, which has a mutation in the regulatory system for an ATP-binding cassette (ABC) transporter gene, forms ectopic spores in substrate hyphae only on glucose-containing medium. In addition, overexpression of a substrate-binding protein of the ABC transporter in the wild-type strain causes ectopic septation in very young substrate hyphae and subsequent sporulation in response to glucose. These ectopic spores germinate normally. The ectopic sporulation is independent of A-factor, a microbial hormone that determines the timing of aerial mycelium formation during normal development. Thus, substrate hyphae of Streptomyces have a potential to develop into spores without formation of aerial hyphae. For programmed development, therefore, the strict repression of septum formation in substrate mycelium should be necessary, as well as the positive signal relay leading to aerial mycelium formation followed by septation and sporulation. (C) 2002 Federation of European Microbiological Societies. Published by Elsevier Science B.V. All rights reserved.

L2 ANSWER 5 OF 20 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2001:806965 SCISEARCH
THE GENUINE ARTICLE: 478BA
TITLE: Improvements in genetic algorithms
AUTHOR: Vasconcelos J A (Reprint); Ramirez J A; Takahashi R H C; Saldanha R R
CORPORATE SOURCE: Univ Fed Minas Gerais, Dept Engn Eletr, Av Antonio Carlos 6627, BR-31270901 Belo Horizonte, MG, Brazil (Reprint); Univ Fed Minas Gerais, Dept Engn Eletr, BR-31270901 Belo Horizonte, MG, Brazil
COUNTRY OF AUTHOR: Brazil
SOURCE: IEEE TRANSACTIONS ON MAGNETICS, (SEP 2001) Vol. 37, No. 5, Part 1, pp. 3414-3417.
Publisher: IEEE-INST ELECTRICAL ELECTRONICS ENGINEERS INC, 345 E 47TH ST, NEW YORK, NY 10017-2394 USA.
ISSN: 0018-9464.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 6

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB This paper presents an exhaustive study of the Simple Genetic Algorithm (SGA), Steady State Genetic Algorithm (**SSGA**) and Replacement Genetic Algorithm (RGA). The performance of each method is analyzed in relation to several operators types of crossover, selection and mutation, as well as in relation to the probabilities of crossover and mutation with and without dynamic change of its values during the optimization process. In addition, the space reduction of the design variables and global elitism are analyzed. All GAS are effective when used with its best operations and values of parameters. For each GA, both sets of best operation types and parameters are found. The dynamic change of crossover and mutation probabilities, the space reduction and the global elitism during the evolution process show that great improvement can be achieved for all GA types. These GAs are applied to TEAM benchmark problem 22.

L2 ANSWER 6 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 2
ACCESSION NUMBER: 2001:407560 CAPLUS
DOCUMENT NUMBER: 135:133005
TITLE: Analysis of a genomic clone of hydrophobin (**ssgA**) from the entomopathogenic fungus Metarhizium anisopliae
AUTHOR(S): Bidochka, Michael J.; De Koning, Jason; St. Leger, Raymond J.
CORPORATE SOURCE: Department of Biology, Trent University, Peterborough, ON, K9J 7B8, Can.
SOURCE: Mycological Research (2001), 105(3), 360-364
CODEN: MYCRER; ISSN: 0953-7562
PUBLISHER: Cambridge University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A 909 bp region contg. a genomic clone encoding for hydrophobin (**ssgA**) from the entomopathogenic fungus Metarhizium anisopliae has been sequenced and the regulatory motifs analyzed against those recognized in other fungi. The genomic clone was also compared with the open reading frame of the hydrophobin **ssgA** (starvation stress gene) cDNA sequence. The genomic clone contained a 291 bp coding sequence with one intron of 64 nucleotides. From this sequence primers were established that could be used to amplify the hydrophobin. Restriction fragment polymorphism anal. of hydrophobin amplified by the polymerase chain reaction from 80 isolates of M. anisopliae showed no variability. Anal. of the potential regulatory elements 313 bp upstream from the transcriptional start site revealed typical TATAA and CCAAT boxes. CT or GC motifs were not found. Upstream regulatory elements were also found with sequence homologies to the AREA, CREA, CRE (cAMP response element) and BRLA regions of Aspergillus nidulans as well as the CYS3 and AmyB regions of Aspergillus oryzae. The promoter regions of other fungal hydrophobins were also assessed for the presence of regulatory elements. Upstream regulatory elements are also present for the gene encoding a cuticle-degrading protease (Pr1) from M. anisopliae. We suggest that nutrient levels and cAMP mediation of thigmotropic signals in the entomopathogenic fungus, M. anisopliae, coordinate the regulation of the gene products required for morphol. development and secretion of "penetration" enzymes.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 3
ACCESSION NUMBER: 2001:465413 CAPLUS
TITLE: Multi-objective evolutionary algorithms for MILP and MINLP in process synthesis
AUTHOR(S): Shi, Lei; Yao, Pingjing
CORPORATE SOURCE: Laboratory of Process System Engineering, Dalian University of Technology, Dalian, 116012, Peop. Rep. China

SOURCE: Chin. J. Chem. Eng. (2001), 9(2), 173-178
CODEN: CJCEEB; ISSN: 1004-9541
PUBLISHER: Chemical Industry Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Steady-state non-dominated sorting genetic algorithm (SNSGA), a new form of multi-objective genetic algorithm, is implemented by combining the steady-state idea in steady-state genetic algorithms (**SSGA**) and the fitness assignment strategy of non-dominated sorting genetic algorithm (NSGA). The fitness assignment strategy is improved and a new self-adjustment scheme of .sigma.shone is proposed. This algorithm is proved to be very efficient both computationally and in terms of the quality of the Pareto fronts produced with five test problems including GA difficult problem and GA deceptive one. Finally, SNSGA is introduced to solve multi-objective mixed integer linear programming (MILP) and mixed integer non-linear programming (MINLP) problems in process synthesis.

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 20 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:719876 CAPLUS
DOCUMENT NUMBER: 136:11692
TITLE: Simultaneous and multi-criteria optimization of TS requirements and maintenance at NPPs
AUTHOR(S): Martorell, S.; Sanchez, A.; Carlos, S.; Serradell, V.
CORPORATE SOURCE: Department of Chemical and Nuclear Engineering, Polytechnical University of Valencia, Valencia, 46071, Spain
SOURCE: Annals of Nuclear Energy (2001), Volume Date 2002, 29(2), 147-168
CODEN: ANENDJ; ISSN: 0306-4549
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB One of the main concerns of the nuclear industry is to improve the availability of safety-related systems at nuclear power plants (NPPs) to achieve high safety levels. The development of efficient testing and maintenance has been traditionally one of the different ways to guarantee high levels of systems availability, which are implemented at NPP through tech. specification and maintenance requirements (TS&M). On the other hand, there is a widely recognized interest in using the probabilistic risk anal. (PRA) for risk-informed applications aimed to emphasize both effective risk control and effective resource expenditures at NPPs. TS&M-related parameters in a plant are assocd. with controlling risk or with satisfying requirements, and are candidates to be evaluated for their resource effectiveness in risk-informed applications. The resource vs. risk-control effectiveness principles formally enter in optimization problems where the cost or the burden for the plant staff is to be minimized while the risk or the availability of the safety equipment is constrained to be at a given level, and vice versa. Optimization of TS&M has been found to be interesting from the very beginning. However, the resoln. of such a kind of optimization problem has been limited to focus on only individual TS&M-related parameters (STI, AOT, PM frequency, etc.) and/or adopting an individual optimization criterion (availability, costs, plant risks, etc.). Nevertheless, a no. of reasons exist (e.g., interaction, similar scope, etc.) that justify the growing interest in the last years to focus on the simultaneous and multi-criteria optimization of TS&M. In the simultaneous optimization of TS&M-related parameters based on risk (or unavailability) and cost, like in many other engineering optimization problems, one normally faces multi-modal and non-linear objective functions and a variety of both linear and non-linear constraints. Genetic algorithms (GAs) have proved their capability to solve these kinds of problems, although GAs are essentially unconstrained optimization techniques that require adaptation for the intended

constrained optimization, where TS&M-related parameters act as the decision variables. This paper encompasses the problem formulation where the objective function is derived and constraints that apply in the simultaneous and multi-criteria optimization of TS&M activities based on risk and cost functions at system level. Fundamentals of a steady-state GA (**SSGA**) as an optimization method are given which satisfies the above requirements, paying special attention to its use in constrained optimization problems. A simple case of application is provided, focusing on TS&M-related parameters optimization for a stand-by safety-related system, which demonstrates how the **SSGA**-based optimization approach works at the system level, providing practical and complete alternatives beyond only math. solns. to a particular parameter.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 9 OF 20 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2001:299474 SCISEARCH
THE GENUINE ARTICLE: 416EA
TITLE: Designing communication networks topologies using steady-state genetic algorithms
AUTHOR: Sayoud H (Reprint); Takahashi K; Vaillant B
CORPORATE SOURCE: Multimedia Univ, CHBN, Fac Engn, Cyberjaya 63100, Malaysia (Reprint)
COUNTRY OF AUTHOR: Malaysia
SOURCE: IEEE COMMUNICATIONS LETTERS, (MAR 2001) Vol. 5, No. 3, pp. 113-115.
Publisher: IEEE-INST ELECTRICAL ELECTRONICS ENGINEERS INC, 345 E 47TH ST, NEW YORK, NY 10017-2394 USA.
ISSN: 1089-7798.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 4

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB This letter presents the application of steady state genetic algorithms (**SSGA**) to minimize the total installation cost of a communication network by optimally designing the topology layout and assigning the corresponding capacities (TDCA problem). This highly constrained optimization problem is shown to be better solved using GA's. A binary representation of links between node pairs is developed and tested on a network of 20 nodes. Improved results, both in terms of network cost, performance and computation speed, are obtained when comparing with existing heuristic approaches.

L2 ANSWER 10 OF 20 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:15369 CAPLUS
DOCUMENT NUMBER: 132:77661
TITLE: Lessening branching and increasing fragmentation when culturing filamentous microorganisms to improve ease of handling
INVENTOR(S): Van Wezel, Gilles Philippus; Kraal, Barend; Luiten, Rudolf Gijsbertus Maria
PATENT ASSIGNEE(S): Rijksuniversiteit te Leiden, Neth.; Nederlandse Organisatie voor Wetenschappelijk Onderzoek/Chemische Wetenschap
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000000613	A1	20000106	WO 1999-NL395	19990625

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

EP 974657 A1 20000126 EP 1998-202148 19980626
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
AU 9946590 A1 20000117 AU 1999-46590 19990625
EP 1090121 A1 20010411 EP 1999-929959 19990625
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
US 2002086412 A1 20020704 US 2000-749185 20001226
PRIORITY APPLN. INFO.: EP 1998-202148 A 19980626
WO 1999-NL395 W 19990625

AB A method of altering the growth habit of filamentous microorganisms in liq. culture to limit branching and increase fragmentation with a consequent improvement in liq. culturing properties is described. This is achieved by introducing the **ssgA** gene of Streptomyces griseus into the microorganism, in particular filamentous fungi. The **ssgA** gene originally found in S. griseus is found in a limited no. of other Streptomycetes, all of which showed sporulation in submerged culture or at least parts of the process. Expression of the gene in Streptomyces coelicolor changed the growth habit from large mycelial lumps to strongly limited branching, frequent septation, and fragmented growth.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 11 OF 20 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2000-04768 BIOTECHDS
TITLE: Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culture properties;
improved Streptomyces griseus recombinant **SsgA** protein production via vector plasmid pGWS2 or plasmid pGWS3-mediated gene transfer and expression in Streptomyces coelicolor
AUTHOR: van Wezel G P; Kraal B; Luiten R G M
PATENT ASSIGNEE: Univ.Leiden; Nederlandse-Org.Wetenschappelijk-Onderzo.
LOCATION: Leiden, The Netherlands; The Hague, The Netherlands.
PATENT INFO: WO 2000000613 6 Jan 2000
APPLICATION INFO: WO 1999-NL395 25 Jun 1999
PRIORITY INFO: EP 1998-202148 26 Jun 1998
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2000-147269 [13]

AB A method (I) for reducing the branching and fragment septation and/or enhancing fragmentation in filamentous bacteria during growth in a liquid culture medium, which involves providing a bacterium that expresses heterologous **SsgA**-activity, which in Streptomyces griseus is encoded by an **ssgA** gene that is encoded by at least a 438 bp DNA sequence (specified), is new. Also claimed are a filamentous bacterium (II) obtained using (I) and a method for producing an antibiotic or useful protein which involves culturing (II) (especially in a submerged culture) and the harvesting the antibiotic or protein from the culture. (I) may be useful for altering the growth of filamentous bacteria in submerged cultures, which may be useful for improving the production of heterologous proteins and products by the bacterium. These products include secondary metabolites such as antibiotics, antitumor agents, immunosuppressive agents, hypocholesterolemic agents,

enzyme-inhibitors, antimigraine agents, herbicides, useful proteins, etc. In an example, vector plasmid pGWS2 and plasmid pGWS3, which contained the **ssgA** gene, were used to transform Streptomyces coelicolor M145 cells. (60pp)

L2 ANSWER 12 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 4
ACCESSION NUMBER: 2000:722097 CAPLUS
DOCUMENT NUMBER: 134:2464
TITLE: **ssgA** is essential for sporulation of Streptomyces coelicolor A3(2) and affects hyphal development by stimulating septum formation
AUTHOR(S): Van Wezel, Gilles P.; Van der Meulen, Jannes; Kawamoto, Shinichi; Luiten, Ruud G. M.; Koerten, Henk K.; Kraal, Barend
CORPORATE SOURCE: Leiden Institute of Chemistry, Leiden University, Leiden, 2300 RA, Neth.
SOURCE: Journal of Bacteriology (2000), 182(20), 5653-5662
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The role of **ssgA** in cell division and development of streptomycetes was analyzed. An **ssgA** null mutant of S. coelicolor produced aerial hyphae but failed to sporulate, and **ssgA** can therefore be regarded as a novel whi gene. In addn. to the morphol. changes, antibiotic prodn. was also disturbed, with strongly reduced actinorhodin prodn. These defects could be complemented by plasmid-borne **ssgA**. In the wild-type strain, transcription of **ssgA** was induced by nutritional shift-down and was shown to be linked to that of the upstream-located gene ssgR, which belongs to the family of iclR-type transcriptional regulator genes. Anal. of mycelium harvested from liq.-grown cultures by transmission electron microscopy showed that septum formation had strongly increased in **ssgA** -overexpressing strains in comparison to wild-type S. coelicolor and that spore-like compartments were produced at high frequency. Furthermore, the hyphae were significantly wider and contained irregular and often extremely thick septa. These data underline the important role for **ssgA** in Streptomyces cell division.
REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 13 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 5
ACCESSION NUMBER: 2000:688832 CAPLUS
DOCUMENT NUMBER: 134:142568
TITLE: Characterization of ssfR and **ssgA**, two genes involved in sporulation of Streptomyces griseus
AUTHOR(S): Jiang, Hao; Kendrick, Kathleen E.
CORPORATE SOURCE: Department of Microbiology, The Ohio State University, Columbus, OH, 43210, USA
SOURCE: Journal of Bacteriology (2000), 182(19), 5521-5529
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In the presence of cefoxitin, which inhibits septum formation during sporulation, Streptomyces griseus is unable to sporulate, retaining the sonication sensitivity of nonsporulating hyphae. Cefoxitin- and sonication-resistant mutant SKK2600 was isolated and showed many morphol. differences from its parental strain. A 3.6-kb DNA fragment that complemented the mutations of SKK2600 contained two open reading frames (ORFs), either of which could complement SKK2600. One ORF, designated ssfR, encoded a protein contg. a potential DNA-binding helix-turn-helix motif close to its N terminus. SsfR is similar to members of a large family of transcriptional regulators, particularly IcIR of Escherichia

coli. The second ORF was identified as **ssgA**, a previously described sporulation gene from S. griseus. A point mutation of C to T seven nucleotides upstream of the UGA stop codon of ssfR was responsible for the phenotype of isolated mutant strain SKK2600. Surprisingly, this mutation should not change the primary structure of SsfR. The ssfR and **ssgA** disruption mutants were constructed and showed the "white" mutant phenotype, with some growth medium dependence. In addn., the ssfR null mutant sporulated ectopically in phosphate starvation medium.
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 14 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 6
ACCESSION NUMBER: 2001:21570 BIOSIS
DOCUMENT NUMBER: PREV200100021570
TITLE: Continuous monitoring of single-sweat-gland activity.
AUTHOR(S): Shamsuddin, A. K. M. (1); Togawa, Tatsuo
CORPORATE SOURCE: (1) Nuclear Medicine Centre, Chittagong Medical College Hospital Campus, Chittagong: akmshams@abnetbd.com Bangladesh
SOURCE: Physiological Measurement, (November, 2000) Vol. 21, No. 4, pp. 535-540. print.
ISSN: 0967-3334.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A conductivity measurement system using a small ion-free-solution perfusion chamber has been developed to monitor single-sweat-gland activity (**SSGA**) continuously at the skin surface. The chamber has a small open space of 0.2 mm2 at the bottom and has a transparent window. Single sweat pores were visualized by the starch/iodine method and the chamber was attached onto a single sweat pore using a magnifying lens affixed at the window. Silver electrodes were installed inside the chamber, and, by perfusing ion-free solution through the chamber at a constant flow rate, the conductivity of the solution was measured at the inlet and the outlet of the chamber. Continuous **SSGA** was monitored at the palm, finger tip and chest skin surface when the subjects were seated in a resting position and under stresses such as hand grasping with a dynamometer and performing mental arithmetic. Different types of response were observed from different sweat pores. The response time of this system was less than 0.15 s. The present results reveal that continuous sweat activity can be monitored even from a single sweat gland.

L2 ANSWER 15 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 7
ACCESSION NUMBER: 2001:407287 CAPLUS
DOCUMENT NUMBER: 135:132924
TITLE: Effects of increased and deregulated expression of cell division genes on the morphology and on antibiotic production of Streptomycetes
AUTHOR(S): van Wezel, Gilles P.; van der Meulen, Jannes; Taal, Elly; Koerten, Henk; Kraal, Barend
CORPORATE SOURCE: Department of Biochemistry, Leiden Institute of Chemistry, Leiden University, Leiden, 2300 RA, Neth.
SOURCE: Antonie van Leeuwenhoek (2000), 78(3-4), 269-276
CODEN: ALJMAO; ISSN: 0003-6072
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
AB This paper describes the effects of increased expression of the cell division genes ftsZ, ftsQ, and **ssgA** on the development of both solid- and liq.-grown mycelium of Streptomyces coelicolor and Streptomyces lividans. Over-expression of ftsZ in S. coelicolor M145 inhibited aerial mycelium formation and blocked sporulation. Such deficient sporulation was also obsd. for the ftsZ mutant. Over-expression of ftsZ also

inhibited morphol. differentiation in S. lividans 1326, although aerial mycelium formation was less reduced. Furthermore, antibiotic prodn. was increased in both strains, and in particular the otherwise dormant actinorhodin biosynthesis cluster of S. lividans was activated in liq.- and solid-grown cultures. No significant alterations were obsd. when the gene dosage of ftsQ was increased. Anal. by transmission electron microscopy of an S. coelicolor strain overexpressing **ssgA** showed that septum formation had strongly increased in comparison to wild-type S. coelicolor, showing that **SsgA** clearly influences Streptomyces cell division. The morphol. of the hyphae was affected such that irregular septa were produced with a significantly wider diam., thereby forming spore-like compartments. This suggests that **ssgA** can induce a process similar to submerged sporulation in Streptomyces strains that otherwise fail to do so. A working model is proposed for the regulation of septum formation and of submerged sporulation.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 16 OF 20 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2000:175072 SCISEARCH
THE GENUINE ARTICLE: 287HW
TITLE: Constrained optimization of test intervals using a steady-state genetic algorithm
AUTHOR: Martorell S (Reprint); Carlos S; Sanchez A; Serradell V
CORPORATE SOURCE: UNIV POLITECN VALENCIA, DEPT INGN QUIM & NUCL, POB 22012, E-46071 VALENCIA, SPAIN (Reprint)
COUNTRY OF AUTHOR: SPAIN
SOURCE: RELIABILITY ENGINEERING & SYSTEM SAFETY, (MAR 2000) Vol. 67, No. 3, pp. 215-232.
Publisher: ELSEVIER SCI LTD, THE BOULEVARD, LANGFORD LANE, KIDLINGTON, OXFORD OX5 1GB, OXON, ENGLAND.
ISSN: 0951-8320.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: ENGI
LANGUAGE: English
REFERENCE COUNT: 42

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB There is a growing interest from both the regulatory authorities and the nuclear industry to stimulate the use of Probabilistic Risk Analysis (PRA) for risk-informed applications at Nuclear Power Plants (NPPs). Nowadays, special attention is being paid on analyzing plant-specific changes to Test Intervals (TIs) within the Technical Specifications (TSs) of NPPs and it seems to be a consensus on the need of making these requirements more risk-effective and less costly. Resource versus risk-control effectiveness principles formally enters in optimization problems. This paper presents an approach for using the PRA models in conducting the constrained optimization of TIs based on a steady-state genetic algorithm (**SSGA**) where the cost or the burden is to be minimized while the risk or performance is constrained to be at a given level, or vice versa. The paper encompasses first with the problem formulation, where the objective function and constraints that apply in the constrained optimization of TIs based on risk and cost models at system level are derived. Next, the foundation of the optimizer is given, which is derived by customizing a **SSGA** in order to allow optimizing TIs under constraints. Also, a case study is performed using this approach, which shows the benefits of adopting both PRA models and genetic algorithms, in particular for the constrained optimization of TIs, although it is also expected a great benefit of using this approach to solve other engineering optimization problems. However, care must be taken in using genetic algorithms in constrained optimization problems as it is concluded in this paper. (C) 2000 Elsevier Science Ltd. All rights reserved.

L2 ANSWER 17 OF 20 SCISEARCH COPYRIGHT 2003 ISI (R)

ACCESSION NUMBER: 1999:536541 SCISEARCH
THE GENUINE ARTICLE: 213EH
TITLE: Identification of a three-amino acid deletion in the alpha(2B)-adrenergic receptor that is associated with reduced basal metabolic rate in obese subjects
AUTHOR: Heinonen P; Koulu M (Reprint); Pesonen U; Karvonen M K; Rissanen A; Laakso M; Valve R; Uusitupa M; Scheinin M
CORPORATE SOURCE: UNIV TURKU, DEPT PHARMACOL & CLIN PHARMACOL, KIINAMYLLYNKATU 10, FIN-20520 TURKU, FINLAND (Reprint); UNIV TURKU, DEPT PHARMACOL & CLIN PHARMACOL, FIN-20520 TURKU, FINLAND; HELSINKI UNIV HOSP, EATING DISORDER UNIT, FIN-00250 HELSINKI, FINLAND; UNIV KUOPIO, DEPT MED, FIN-70211 KUOPIO, FINLAND; UNIV KUOPIO, DEPT CLIN NUTR, FIN-70211 KUOPIO, FINLAND
COUNTRY OF AUTHOR: FINLAND
SOURCE: JOURNAL OF CLINICAL ENDOCRINOLOGY AND METABOLISM, (JUL 1999) Vol. 84, No. 7, pp. 2429-2433.
Publisher: ENDOCRINE SOC, 4350 EAST WEST HIGHWAY SUITE 500, BETHESDA, MD 20814-4110.
ISSN: 0021-972X.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 29
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The alpha(2)-adrenergic receptors mediate part of the actions of the catecholamines noradrenaline and adrenaline on the regulation of energy balance. As part of an ongoing study on the genetics of obesity, the entire coding sequence of the alpha(2B)-adrenoceptor gene was screened in 58 obese, nondiabetic Finns by FOR-single stranded conformational analysis (PGR-**SSGA**). A polymorphism that leads to a deletion of 3 glutamic acids from a glutamic acid repeat element (Glu x 12, amino acids 297-309) present in the third intracellular loop of the receptor protein was identified. This repeat element has previously been shown to be important for agonist-dependent receptor desensitization. Of 166 genotyped subjects, 47 (28%) had 2 normal (long) alleles (Glu(12)/Glu(12)), 90 (54%) were heterozygous (Glu(12)/Glu(9)), and 29 (17%) were homozygous for the short (Glu(9)/Glu(9)) form. The basal metabolic rate, determined by indirect calorimetry and adjusted for fat-free body mass, fat mass, sex, and age, was 94 Cal/day (5.6%) lower (95% confidence interval for difference, 32, 156) in subjects homozygous for the short allele than in subjects with two long alleles (F = 4.84; P = 0.009, by ANOVA). Thus, a genetic polymorphism of the alpha(2B)-adrenoceptor subtype can partly explain the variation in basal metabolic rate in an obese population and may therefore contribute to the pathogenesis of obesity.

L2 ANSWER 18 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 8
ACCESSION NUMBER: 1998:518346 CAPLUS
DOCUMENT NUMBER: 129:200360
TITLE: Complementation of the Mpg1 mutant phenotype in Magnaporthe grisea reveals functional relationships between fungal hydrophobins
AUTHOR(S): Kershaw, Michael J.; Wakley, Gavin; Talbot, Nicholas J.
CORPORATE SOURCE: Department of Biological Sciences, Washington Singer Laboratories, University of Exeter, Exeter, EX4 4QG, UK
SOURCE: EMBO Journal (1998), 17(14), 3838-3849
CODEN: EMJODG; ISSN: 0261-4189
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The functional relationship between fungal hydrophobins was studied by complementation anal. of an mpg1- gene disruption mutant in Magnaporthe

grisea. MPG1 encodes a hydrophobin required for full pathogenicity of the fungus, efficient elaboration of its infection structures and conidial rodlet protein prodn. Seven heterologous hydrophobin genes were selected which play distinct roles in conidiogenesis, fruit body development, aerial hyphae formation and infection structure elaboration in diverse fungal species. Each hydrophobin was introduced into an mpg1- mutant by transformation. Only one hydrophobin gene, SC1 from Schizophyllum commune, was able partially to complement mpg1- mutant phenotypes when regulated by its own promoter. In contrast, six of the transformants expressing hydrophobin genes controlled by the MPG1 promoter (SC1 and SC4 from S.commune, rodA and dewA from Aspergillus nidulans, EAS from Neurospora crassa and **ssgA** from Metarhizium anisopliae) could partially complement each of the diverse functions of MPG1. Complementation was always assocd. with partial restoration of a rodlet protein layer, characteristic of the particular hydrophobin being expressed, and with hydrophobin surface assembly during infection structure formation. This provides the first genetic evidence that diverse hydrophobin-encoding genes encode functionally related proteins and suggests that, although very diverse in amino acid sequence, the hydrophobins constitute a closely related group of morphogenetic proteins.
REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 19 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 9
ACCESSION NUMBER: 1997:301915 CAPLUS
DOCUMENT NUMBER: 127:15298
TITLE: Expression analysis of the **ssgA** gene product, associated with sporulation and cell division in Streptomyces griseus
AUTHOR(S): Kawamoto, Shinichi; Watanabe, Hajime; Hesketh, Andrew; Ensign, Jerald C.; Ochi, Kozo
CORPORATE SOURCE: National Food Research Institute, Ibaraki, 305, Japan
SOURCE: Microbiology (Reading, United Kingdom) (1997), 143(4), 1077-1086
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The **ssgA** gene of Streptomyces griseus B2682, when present in high copy no., results in both suppression of sporulation and fragmented growth of mycelia. Western anal. with polyclonal antibodies against the gene product (**SsgA**) revealed a close correlation between **SsgA** accumulation and the onset of sporulation in wild-type cells. The protein was only detected in the cytoplasm. Certain developmental mutants of S. griseus (afs, relC and brgA) which are defective in aerial mycelium formation in solid culture and submerged spore formation in liq. culture failed to accumulate **SsgA**. The **SsgA** protein appeared shortly (1 h) after nutritional shift-down of strain B2682 cells. Afs mutant cells sporulated and expressed **SsgA** only when A-factor was present both before and after nutritional shift-down. Introduction of the **ssgA** gene in a low-copy-no. vector into strain B2682 resulted in fivefold overexpression of **SsgA**, and was accompanied by fragmented growth of mycelia and suppression of submerged spore formation (in liq. culture) and aerial mycelium formation (in solid culture). Streptomycin prodn. was not inhibited. In a control expt., a nonfunctional **ssgA** gene possessing a frameshift mutation near its N-terminus had no effect on either growth or sporulation. It is proposed that the **ssgA** gene product plays a role in promoting the developmental process of S. griseus.

L2 ANSWER 20 OF 20 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 10
ACCESSION NUMBER: 1993:465878 CAPLUS
DOCUMENT NUMBER: 119:65878
TITLE: Cloning and regulatory analysis of starvation-stress

gene, **ssgA**, encoding a hydrophobin-like protein from the entomopathogenic fungus, Metarhizium anisopliae

AUTHOR(S): St. Leger, Raymond J.; Staples, Richard C.; Roberts, Donald W.

CORPORATE SOURCE: Boyce Thompson Inst. Plant Res., Inc., Ithaca, NY, 14853-1801, USA

SOURCE: Gene (1992), 120(1), 119-24
CODEN: GENED6; ISSN: 0378-1119

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The nucleotide (nt) sequence of a starvation-stress gene (**ssgA**) of the entomopathogenic fungus, M. anisopliae, and its deduced amino acid (aa) sequence were detd. The primary structure of the **SSGA** (96 aa; deduced Mr = 9925; pI = 4.1) protein shares extensive similarities with fungal wall proteins of the hydrophobin class, and the eight Cys residues and putative signal sequences are conserved. Secondary structure predictions suggest an addnl. resemblance to low-Mr toxins and agglutinins. Northern (RNA) blot anal. and nuclear run-on assays demonstrated transcriptional control of expression of **ssgA** during nutrient deprivation and during formation of infection structures. Hybridizations of M. anisopliae genomic DNA indicate that there is only one form of **ssgA** in the genome.

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=> d his

     (FILE 'HOME' ENTERED AT 09:43:06 ON 22 JAN 2003)

     FILE 'CAPLUS, BIOSIS, EMBASE, MEDLINE, SCISEARCH, BIOTECHNO, BIOTECHDS'
     ENTERED AT 09:43:44 ON 22 JAN 2003
L1            62 S SSGA
L2            20 DUP REM L1 (42 DUPLICATES REMOVED)
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End of Result Set

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L1: Entry 18 of 18 File: DWPI Jan 6, 2000

DERWENT-ACC-NO: 2000-147269
DERWENT-WEEK: 200247

TITLE: Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties

Basic Abstract Text (1):
NOVELTY - Novel method (I) for reducing branching and fragment septation and/or enhancing fragmentation in filamentous bacteria during growth in a liquid medium. Comprises providing a bacterium that has or expresses heterologous SsgA-activity, which in Streptomyces griseus is encoded by a ssgA gene that has at least a 438 bp sequence (fully defined in the specification).

Basic Abstract Text (6):
ADVANTAGE - (I) allows easy integration of the ssgA gene into the chromosome of the bacterium, resulting in high stability and independent regulation of ssgA. In this way, (I) reduces branching and fragment septation and enhances fragmentation of the mycelium in liquid culture, resulting in lower viscosity of culture broths and allowing high yields of useful products produced by the bacteria to be maintained.

Equivalent Abstract Text (1):
NOVELTY - Novel method (I) for reducing branching and fragment septation and/or enhancing fragmentation in filamentous bacteria during growth in a liquid medium. Comprises providing a bacterium that has or expresses heterologous SsgA-activity, which in Streptomyces griseus is encoded by a ssgA gene that has at least a 438 bp sequence (fully defined in the specification).

Equivalent Abstract Text (6):
ADVANTAGE - (I) allows easy integration of the ssgA gene into the chromosome of the bacterium, resulting in high stability and independent regulation of ssgA. In this way, (I) reduces branching and fragment septation and enhances fragmentation of the mycelium in liquid culture, resulting in lower viscosity of culture broths and allowing high yields of useful products produced by the bacteria to be maintained.

Search Results - Record(s) 1 through 18 of 18 returned.

☐ 1. Document ID: US 20020086412 A1

L1: Entry 1 of 18 File: PGPB Jul 4, 2002

PGPUB-DOCUMENT-NUMBER: 20020086412
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020086412 A1

TITLE: Reducing branching and enhancing fragmentation in culturing filamentous microorganisms

PUBLICATION-DATE: July 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
van Wezel, Gilles Philippus	Leiden		NL	
Kraal, Barend	Leiden		NL	
Luiten, Rudolf Gijsbertus, M.	Leiden		NL	

US-CL-CURRENT: 435/252.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 2. Document ID: US 6272465 B1

L1: Entry 2 of 18 File: USPT Aug 7, 2001

US-PAT-NO: 6272465
DOCUMENT-IDENTIFIER: US 6272465 B1

TITLE: Monolithic PC audio circuit

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 3. Document ID: US 6246774 B1

L1: Entry 3 of 18 File: USPT Jun 12, 2001

US-PAT-NO: 6246774
DOCUMENT-IDENTIFIER: US 6246774 B1

TITLE: Wavetable audio synthesizer with multiple volume components and two modes of stereo positioning

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 4. Document ID: US 6064743 A

L1: Entry 4 of 18 File: USPT May 16, 2000

US-PAT-NO: 6064743
DOCUMENT-IDENTIFIER: US 6064743 A

TITLE: Wavetable audio synthesizer with waveform volume control for eliminating zipper noise

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

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☐ 5. Document ID: US 6058066 A

L1: Entry 5 of 18 File: USPT May 2, 2000

US-PAT-NO: 6058066
DOCUMENT-IDENTIFIER: US 6058066 A

TITLE: Enhanced register array accessible by both a system microprocessor and a wavetable audio synthesizer

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 6. Document ID: US 6047073 A

L1: Entry 6 of 18 File: USPT Apr 4, 2000

US-PAT-NO: 6047073
DOCUMENT-IDENTIFIER: US 6047073 A

TITLE: Digital wavetable audio synthesizer with delay-based effects processing

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 7. Document ID: US 5864024 A

L1: Entry 7 of 18 File: USPT Jan 26, 1999

US-PAT-NO: 5864024
DOCUMENT-IDENTIFIER: US 5864024 A

TITLE: Synthetic glycoamines and methods for their use that affect cell adhesion, inhibit cancer cell metastasis, and induce apoptosis

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 8. Document ID: US 5809466 A

L1: Entry 8 of 18 File: USPT Sep 15, 1998

US-PAT-NO: 5809466
DOCUMENT-IDENTIFIER: US 5809466 A

TITLE: Audio processing chip with external serial port

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 9. Document ID: US 5742695 A

L1: Entry 9 of 18 File: USPT Apr 21, 1998

US-PAT-NO: 5742695
DOCUMENT-IDENTIFIER: US 5742695 A

TITLE: Wavetable audio synthesizer with waveform volume control for eliminating zipper noise

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 10. Document ID: US 5717787 A

L1: Entry 10 of 18 File: USPT Feb 10, 1998

US-PAT-NO: 5717787
DOCUMENT-IDENTIFIER: US 5717787 A

TITLE: Method for data compression by associating complex numbers with files of data values

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 11. Document ID: US 5675808 A

L1: Entry 11 of 18 File: USPT Oct 7, 1997

US-PAT-NO: 5675808
DOCUMENT-IDENTIFIER: US 5675808 A

TITLE: Power control of circuit modules within an integrated circuit

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 12. Document ID: US 5668338 A

L1: Entry 12 of 18 File: USPT Sep 16, 1997

US-PAT-NO: 5668338
DOCUMENT-IDENTIFIER: US 5668338 A

TITLE: Wavetable audio synthesizer with low frequency oscillators for tremolo and vibrato effects

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 13. Document ID: US 5659466 A

L1: Entry 13 of 18 File: USPT Aug 19, 1997

US-PAT-NO: 5659466
DOCUMENT-IDENTIFIER: US 5659466 A

TITLE: Monolithic PC audio circuit with enhanced digital wavetable audio synthesizer

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 14. Document ID: US 5629412 A

L1: Entry 14 of 18 File: USPT May 13, 1997

US-PAT-NO: 5629412
DOCUMENT-IDENTIFIER: US 5629412 A

TITLE: Synthetic glycoamines that promote or inhibit cell adhesion

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments KWIC | Draw Desc | Image

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☐ 15. Document ID: US 4887049 A

L1: Entry 15 of 18 File: USPT Dec 12, 1989

US-PAT-NO: 4887049
DOCUMENT-IDENTIFIER: US 4887049 A

TITLE: Solid state space harmonic amplifier

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments KWIC | Draw Desc | Image

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☐ 16. Document ID: JP 61258534 A

L1: Entry 16 of 18 File: JPAB Nov 15, 1986

PUB-NO: JP361258534A
DOCUMENT-IDENTIFIER: JP 61258534 A
TITLE: DIGITAL SIGNAL DEMODULATOR

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments KWIC | Draw Desc | Image

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☐ 17. Document ID: EP 974657 A1

L1: Entry 17 of 18 File: EPAB Jan 26, 2000

PUB-NO: EP000974657A1
DOCUMENT-IDENTIFIER: EP 974657 A1
TITLE: Reducing branching and enhancing fragmentation in culturing filamentous microorganisms

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments KWIC | Draw Desc | Image

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☐ 18. Document ID: WO 200000613 A1 US 20020086412 A1 EP 974657 A1 AU 9946590 A EP 1090121 A1

L1: Entry 18 of 18 File: DWPI Jan 6, 2000

DERWENT-ACC-NO: 2000-147269
DERWENT-WEEK: 200247

TITLE: Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments KWIC | Draw Desc | Image

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Terms	Documents
ssgA	18

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